General

OP-119

Vitamin A Supplementation Effects on Gene Expression of Cytokines Secreted by TCD4+ Lymphocytes in Atherosclerotic Patients

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Aim: Atherosclerosis is an inflammatory arterial wall disease and T lymphocytes have important role in the pathogenesis and progression of this disease. The aim of this study is determination of vitamin A supplementation effects on gene expression of cytokines secreted by TCD4+ lymphocytes in atherosclerotic patients.
Methods-Materials: Thirty one atherosclerotic patients and 12 healthy controls participated in this study. Patients were randomly divided into vitamin A receiving group (n=16) and placebo receiving group (n=15), also healthy controls were receiving vitamin A. vitamin A supplement was given as retinyl palmitate and 25000 IU per day. Fasting blood sample of participants were taken before and after 4 months and plasma was separated and stored at -80 0C for biochemical laboratory tests. Peripheral blood mononuclear cells (PBMC) were separated and cultured in the appropriate number along with PHA and ox-LDL for proliferation assay and determination of gene expression pattern. As well as RNA was extracted and cDNA was synthesized from part of the cells at the same time and was stored for Real-Time PCR analysis. After 72 hour incubation cells supernatant were collected and stored at-800C; cells deposited were collected for PNA extraction and cDNA synthesis. After the intervention period the gene expression pattern of relevant cytokines of CD4+ T cells including Th1, Th2, Th17 and Treg were determined by Real-Time PCR.
Results: There was significant difference in fasting blood sugar, total cholesterol and LDL cholesterol between three groups of study, before and after intervention. Vitamin A increased proliferation of cells that stimulated with ox-LDL in all groups. Results of this study show that IFN-y and T- bet gene expression in fresh cells in vitamin A-treated patients was decreased. The IL-4 gene expression was increased 12.7 fold in vitamin A-treated patients. IL-17 gene expression in fresh cells of vitamin A-treated patients was diminished. Foxp3 gene expression in fresh cells was increased after intervention in all groups.
Conclusion: vitamin A supplementation had no significant effect on anthropometric factors and effect of this intervention on biochemical factors limited to increase in total cholesterol and HDL cholesterol in both groups of patients and controls but the amounts were in normal value ranges. Vitamin A supplementation could reduce gene expression of IFN-y T-bet in all patients. Increase in gene expression of Th2 cells was seen in all group expect GATA3 gene. According to the results of how the effect of vitamin A on gene expression in atherosclerotic patients, perhaps we thought the positive role of vitamin A supplementation in these patients. Results of this study could pave the way for a more detailed review on effect of vitamin A in patients with immune related diseases.

OP-120

Beta Fibrinogen -455 G>A Gene Polymorphism in Coronary Artery Ectasia

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Background: Coronary artery ectasia (CAE) is defined as local or generalized aneurysmal dilatation of the coronary arteries. Although the etiology of CAE has not been identified completely, the most frequent cause is coronary atherosclerosis. It is known that an expansive remodelling occurs in atherosclerotic coronary arteries due to plague rupture and increased plague burden particularly in early stages. β-fibrinogen -455 G/A genotypes have been described to be associated with coronary artery disease and myocardial infarction. Although various gene polymorphsims have been studied in patients with CAE, β-fibrinogen gene polymorphisms have not been studied previously. We investigated relationship between β-fibrinogen -455 G>A gene polymorphism and CAE.
Methods: Sixty five patients with isolated CAE (mean age 53±7 years) and 65 controls with normal coronary angiograms (mean age 51±7 years) were included in the study. The types of β-fibrinogen -455 G>A gene polymorphisms were analysed by polymerase chain reaction and restriction fragment length polymorphism. For each polymorphic position, one of three possible patterns may be obtained: Normal (GG) genotype, heterozygous (GA), or homozygous (AA) mutant genotype. Demographic characteristics and major risk factors for atherosclerosis were evaluated in the study groups.
Results: There was no significant difference with respect to age and gender between groups. The frequency of the GA heterozygous genotype was significantly higher in CAE group than controls (39 (60%) vs 25 (38.5%), p=0.014). Between the two groups were compared according to the dominant genetic model (GA+AA vs. GG), The number of patients carrying at least one A mutant allele (GA+AA) were significantly higher in CAE than controls (44 (67.7%) vs 26 (40%), p=0.002). With respect to allelic distribution (G vs A, additive model), the frequency of the A mutant allele was significantly higher in CAE patients. (49 (37.6%) vs 27 (20.7%), p=0.004).
Conclusions: In this study, we found that the frequency of β-fibrinogen -455 G>A polymorphism was higher in patients with CAE compared to control subject. However, further large-sized studies are required for determining relationship between β-fibrinogen – 455 G>A gene polymorphisms and CAE.

OP-121

Evaluation of Endothelial Nitric Oxide Synthase Gene Polymorphism (T-786 C) in Patients with Slow Coronary Flow

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Background: Slow coronary flow (SCF) is characterized by delay of opacification of coronary arteries in coronary angiography in the absence of any evident obstructive lesion. Its pathophysiological mechanisms are uncertain. Several hypotheses have been suggested for SCF, including a form of early phase of atherosclerosis, microvascular dysfunction, inflammation, imbalance between vasoconstrictor and vasodilatory factors, and platelet function disorder. Endothelial nitric oxide synthase (eNOS) gene T-786 C polymorphism have been reported to be associated with many vascular disease.
Objective: The aim of this study was to investigate the association between SCF and eNOS gene T-786 C polymorphism.
Methods: Forty patients with SCF and otherwise normal coronary arteries (mean age 52±9 years), 35 patients with coronary artery disease (CAD) (mean age 55±9 years) and 30 patients with normal coronary angiograms (mean age 51±8 years) were included in the study. TIMI frame count ≥40 frames for the left anterior descending artery was considered as SCF. T-786 C polymorphisms of the eNOS gene were analysed by polymerase chain reaction. Demographic characteristics and major risk factors for atherosclerosis were evaluated in the study groups. The severity of SCF and CAD was assessed based on the number of involved vessel.
Results: There was no significant difference with respect to age and gender between groups. The percentage of smoking was higher in the CAD group than in the SCF and control groups. There was no statistical difference in genotype distribution among the groups. The genotype distribution in SCF group was as follows: TT genotype frequency was 25 (62,5%)k, TC genotype frequency was 12 (30%) and CC genotype frequency was 3 (7,5%). The genotype distribution in CAD group was as follows: TT genotype frequency was 16 (45,7%), TC genotype frequency was 16 (45,7%) and CC genotype frequency was 3 (8,5%). The genotype distribution in control group was as follows: TT genotype frequency was 17 (56,6%), TC genotype frequency was 10 (33,3%) and CC genotype frequency was 3 (10%). In the dominant and recessive models of statistical analysis, there was no statistically significant difference among groups.
Conclusions: Our findings show that there is no significant association between T-786 C polymorphism of eNOS gene and SCF in the present study.

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Lack of Association between the Glu298Asp Polymorphism of Endothelial Nitric Oxide Synthase and Slow Coronary Flow

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Background: Slow coronary flow (SCF) is slow progression of contrast agent in the coronary arteries in the absence of stenosis in epicardial coronary vessels. Its pathophysiological mechanisms are uncertain. Several hypotheses have been suggested for SCF, including a form of early phase of atherosclerosis, microvascular dysfunction, inflammation, imbalance between vasoconstrictor and vasodilatory factors, and platelet function disorder. Endothelial nitric oxide synthase (eNOS) has important role in modulating smooth muscle tonus and vessel diameter. eNOS gene Glu298Asp polymorphism has been associated with altered function of this gene and its products. Experimental and clinical data suggesting that; in the absence of eNOS, endothelial functions and luminal remodeling is impaired, the vessel wall thickness is increased, atherosclerosis accelerated and got complicated.
Objective: The aim of this study was to investigate the association between SCF and eNOS gene Glu298Asp polymorphism.
Methods: Forty patients with SCF and otherwise normal coronary arteries (mean age 52±9 years), 35 patients with coronary artery disease (CAD) (mean age 55±9 years) and 30 patients with normal coronary angiograms (mean age 51±8 years) were included in the study. TIMI frame count ≥40 frames for the left anterior descending artery was considered as SCF. Glu298Asp polymorphisms of the eNOS gene were